

004770" 889E3460

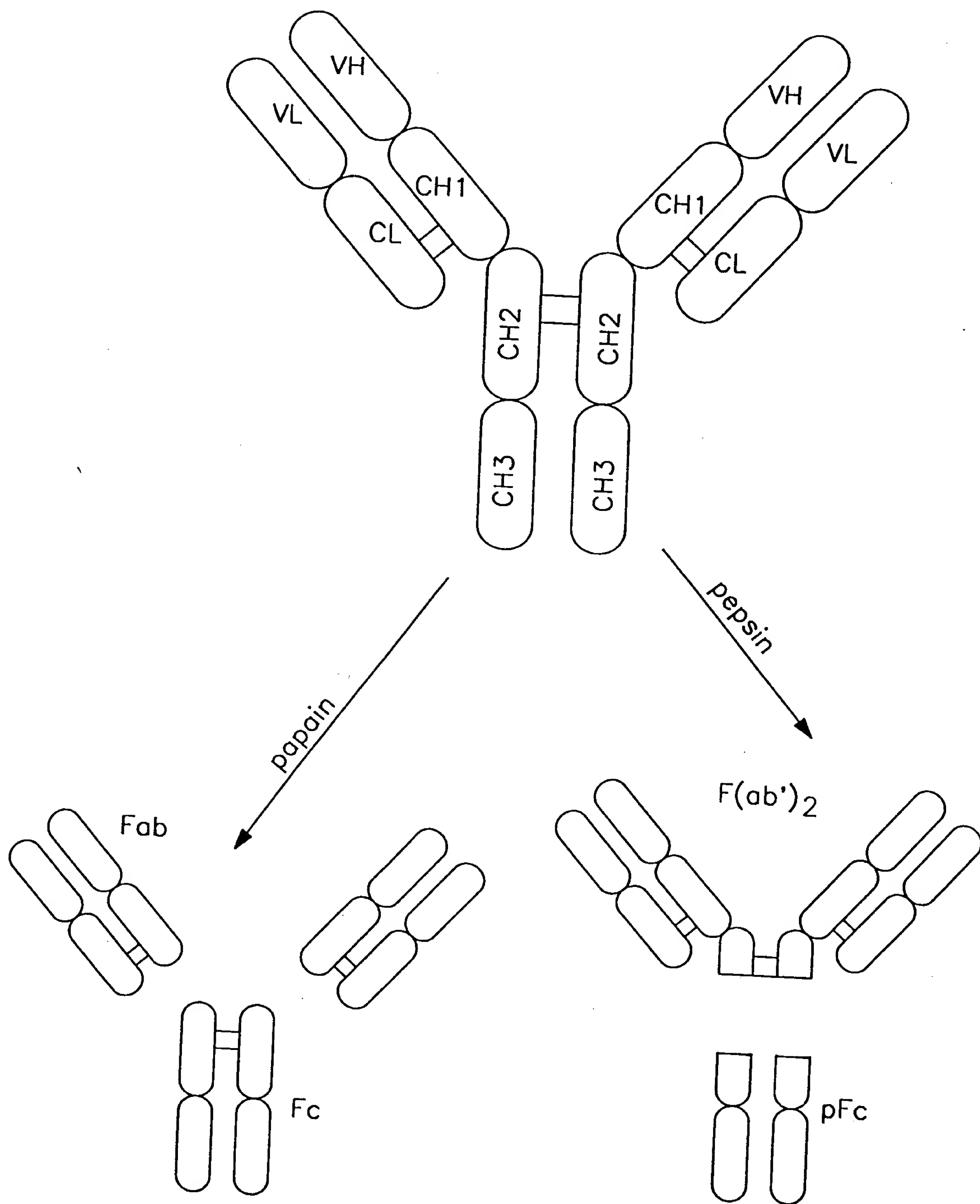


FIG. 1

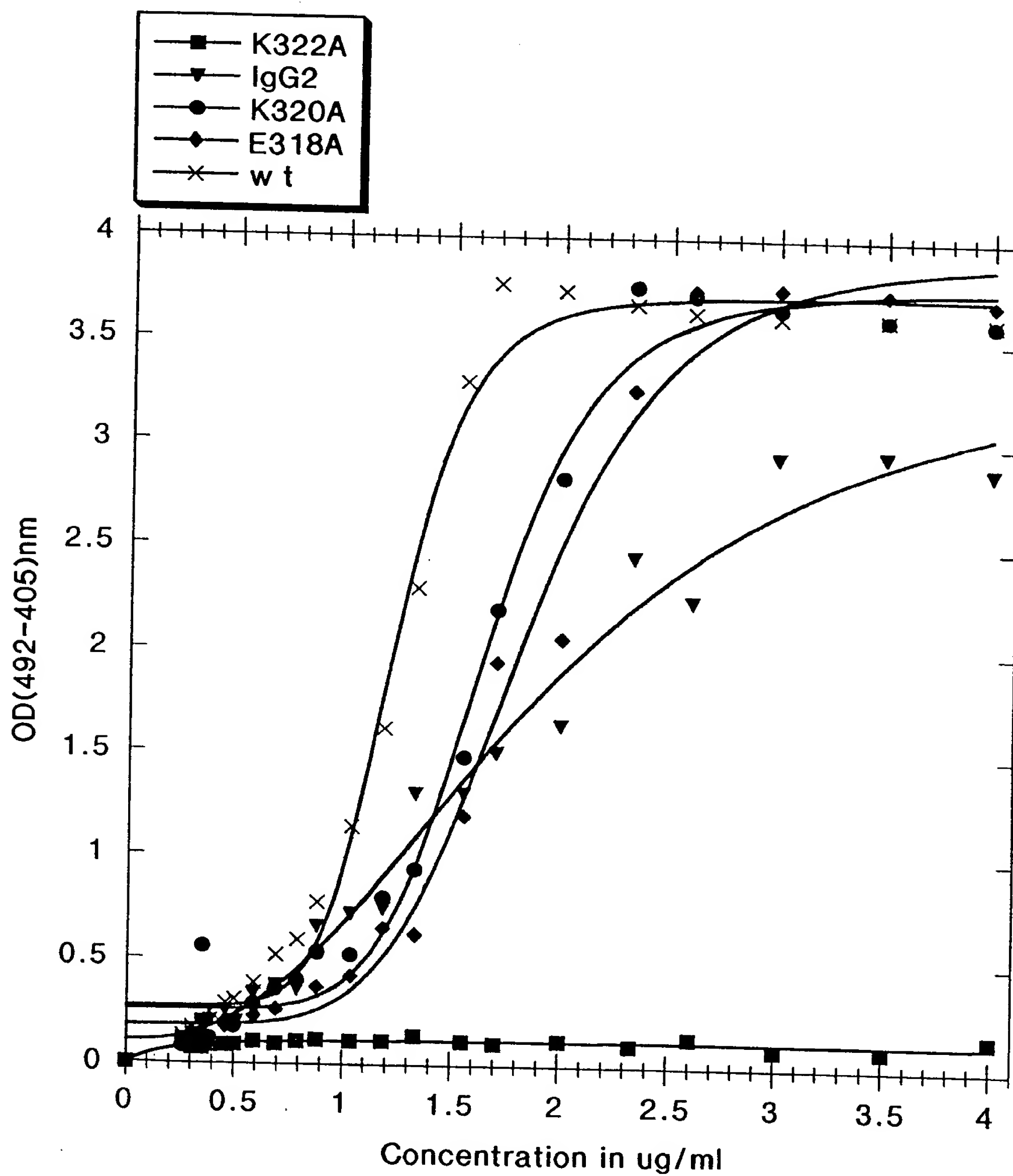


FIG. 2

001170" 8852460

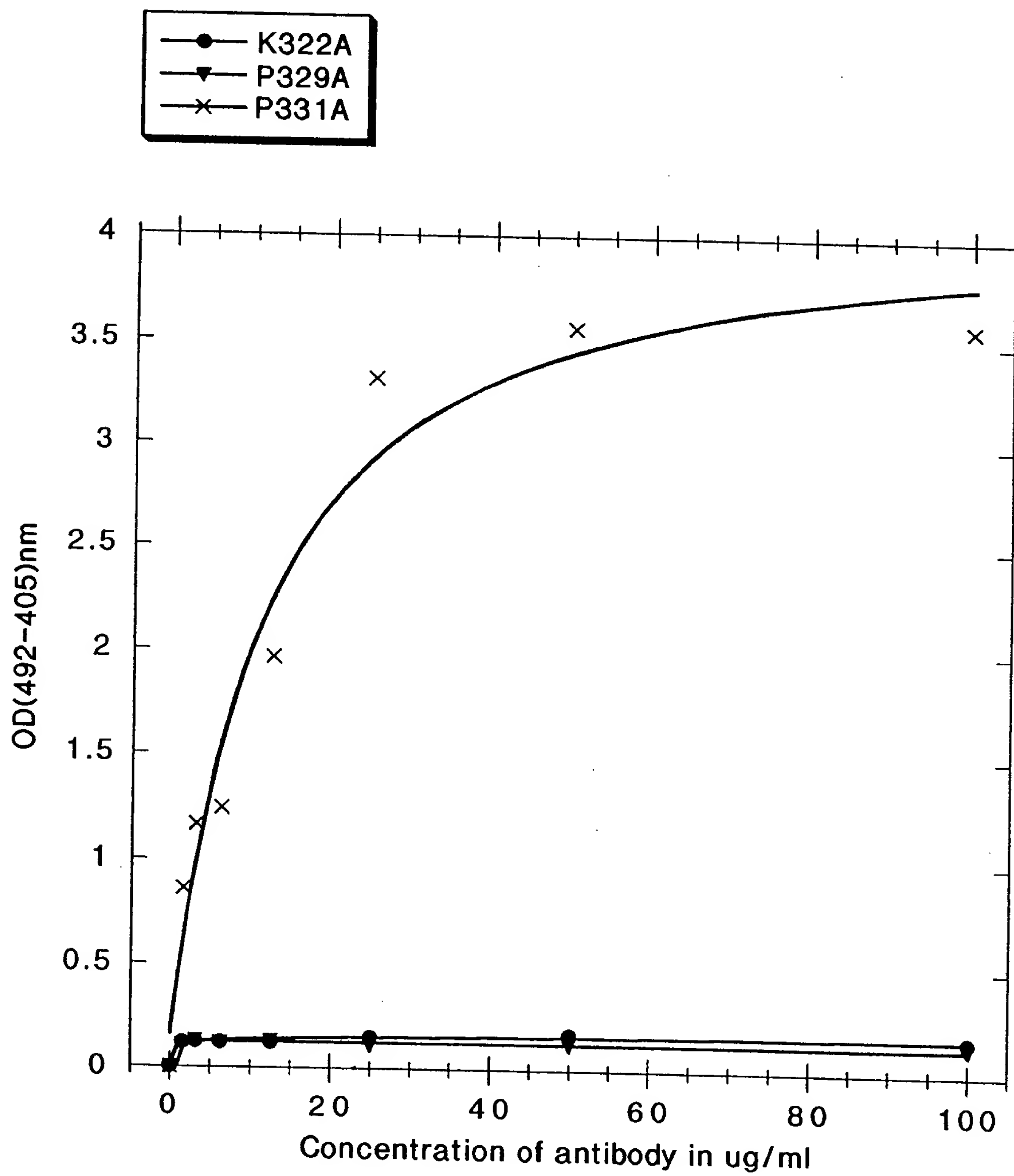


FIG. 3

FIG. 4A (E27) - Light Chain

DIQLTQSPSS LSASVGDRVT ITCRASKPVD GEGDSYMNWY QKPGKAPKL LIYAASYLES GVPSRFSGSG  
SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL  
NNFYPPREKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLKADY EKHKVYACEV THQGLSSPVT  
KSFNRGEC

FIG. 4B (E27) - Heavy Chain

EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SIKYSGETKY NPSVKGRITI  
SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFAV WQQTGLVTVS SASTKGPSVF PLAPSSKSTS  
GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSV TVPSSSLGTQ TYICNVNHKP  
SNTKVDKKVE PKSCDKTHC PPCPAPELLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN  
WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP  
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTPP VLDSGGSFFL YSKLTVDKSR  
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K

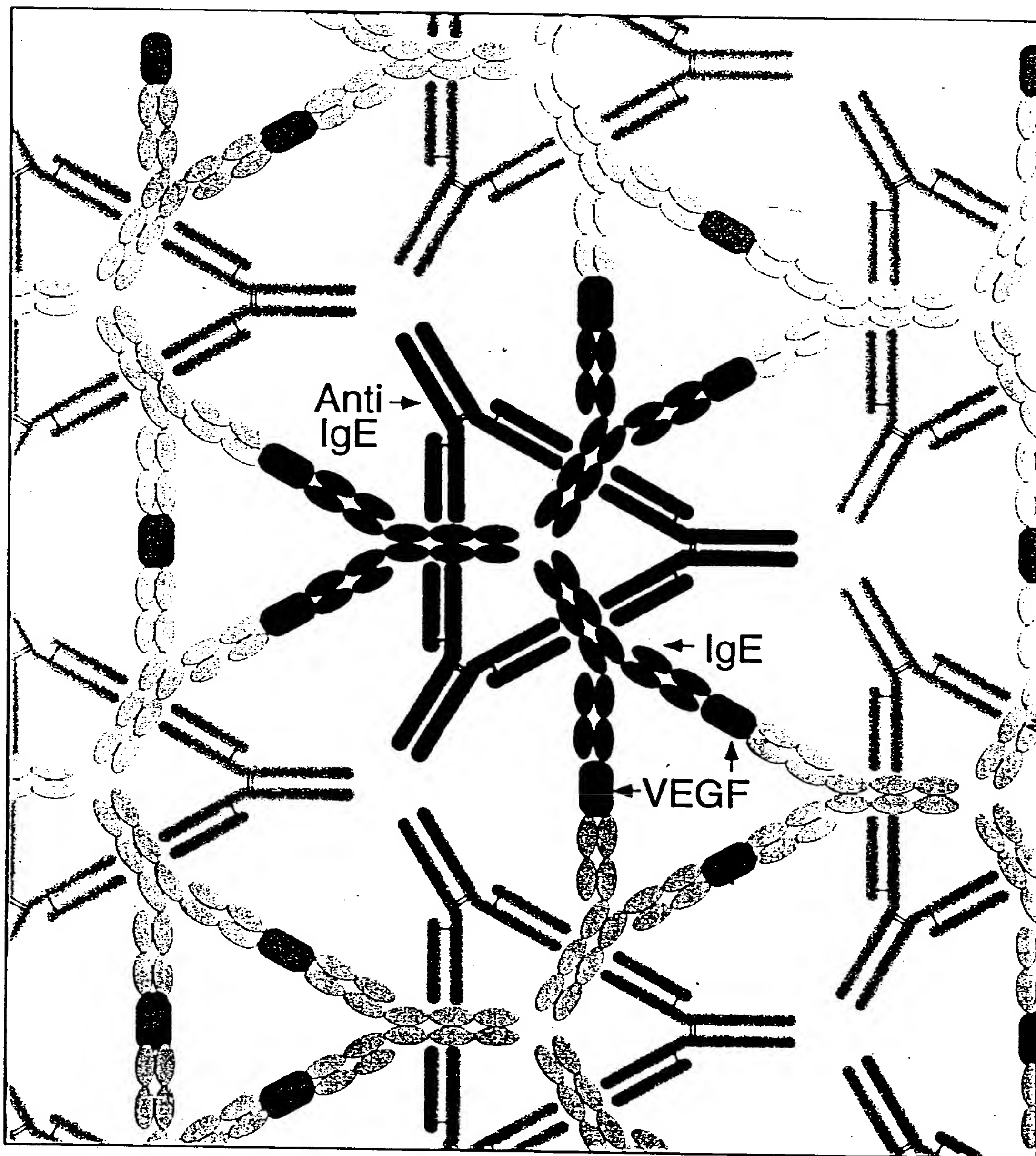


Fig. 5

00470-8856460

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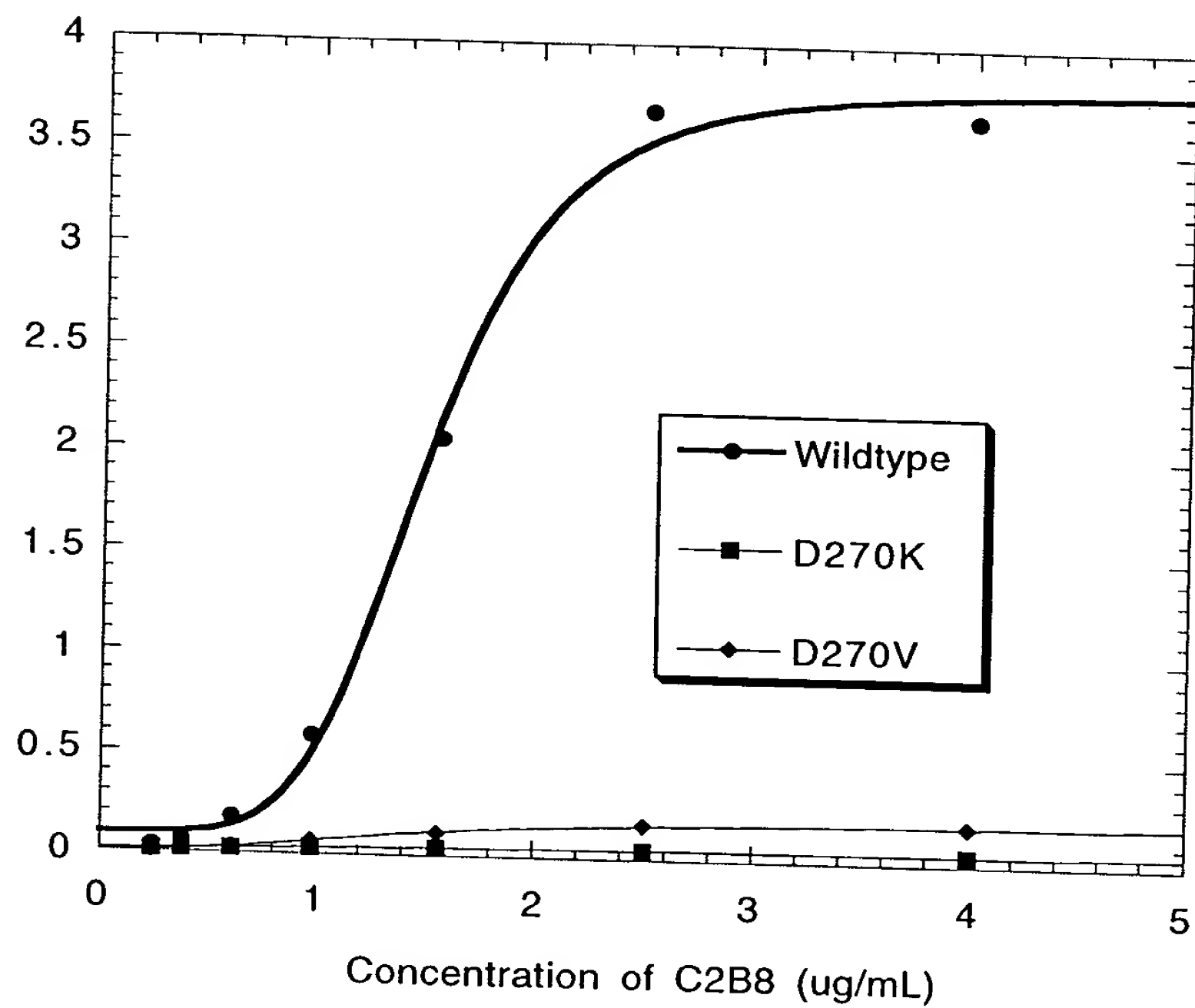


FIG. 6

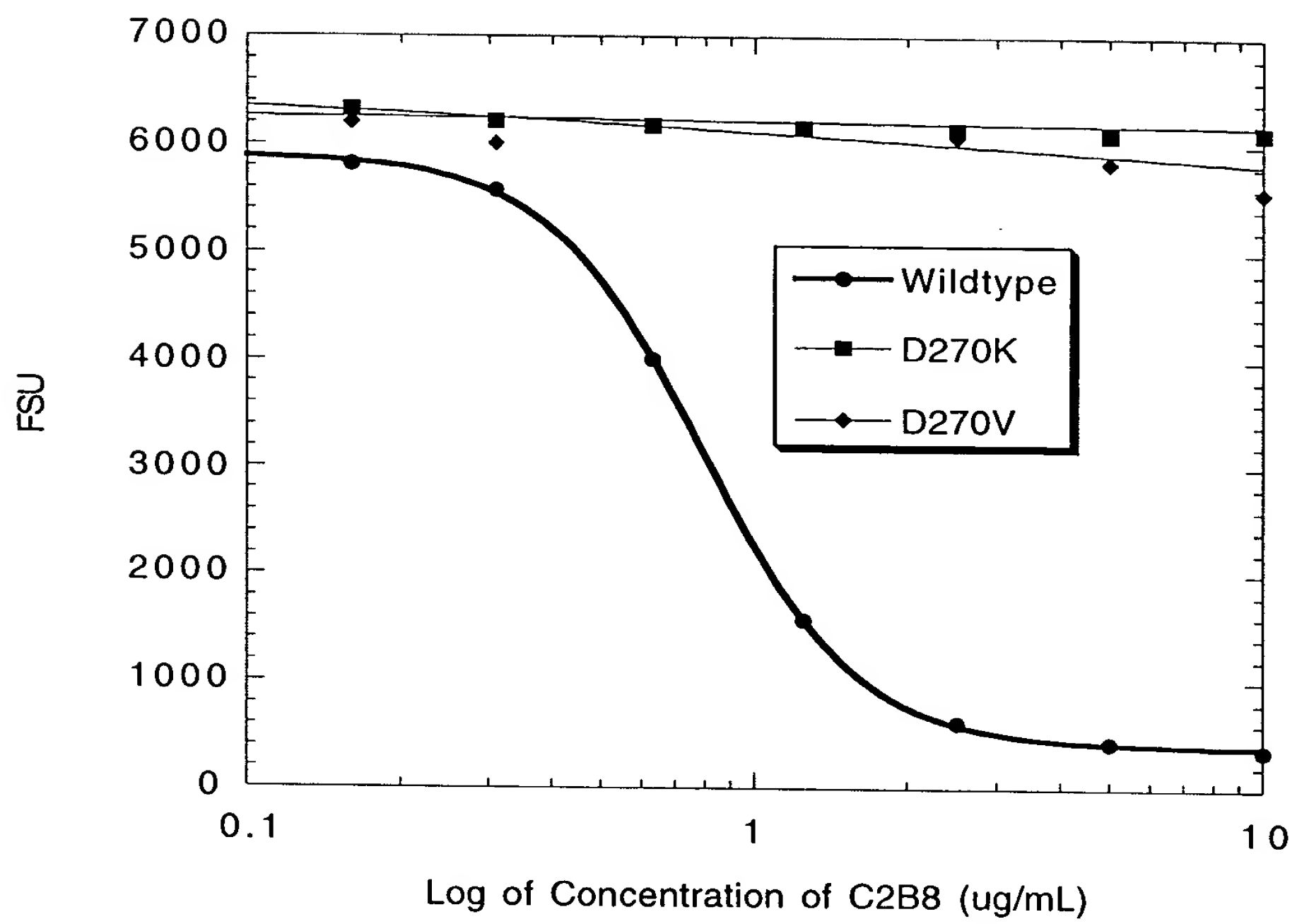


FIG. 7

- K274A
- S324A
- ◇— K326A
- ×— K334A
- +— P329A
- P331A
- E333A
- ◆— 293-Wt-C2B8
- CHO-Wt-C2B8
- ▲— Y278A
- T335A

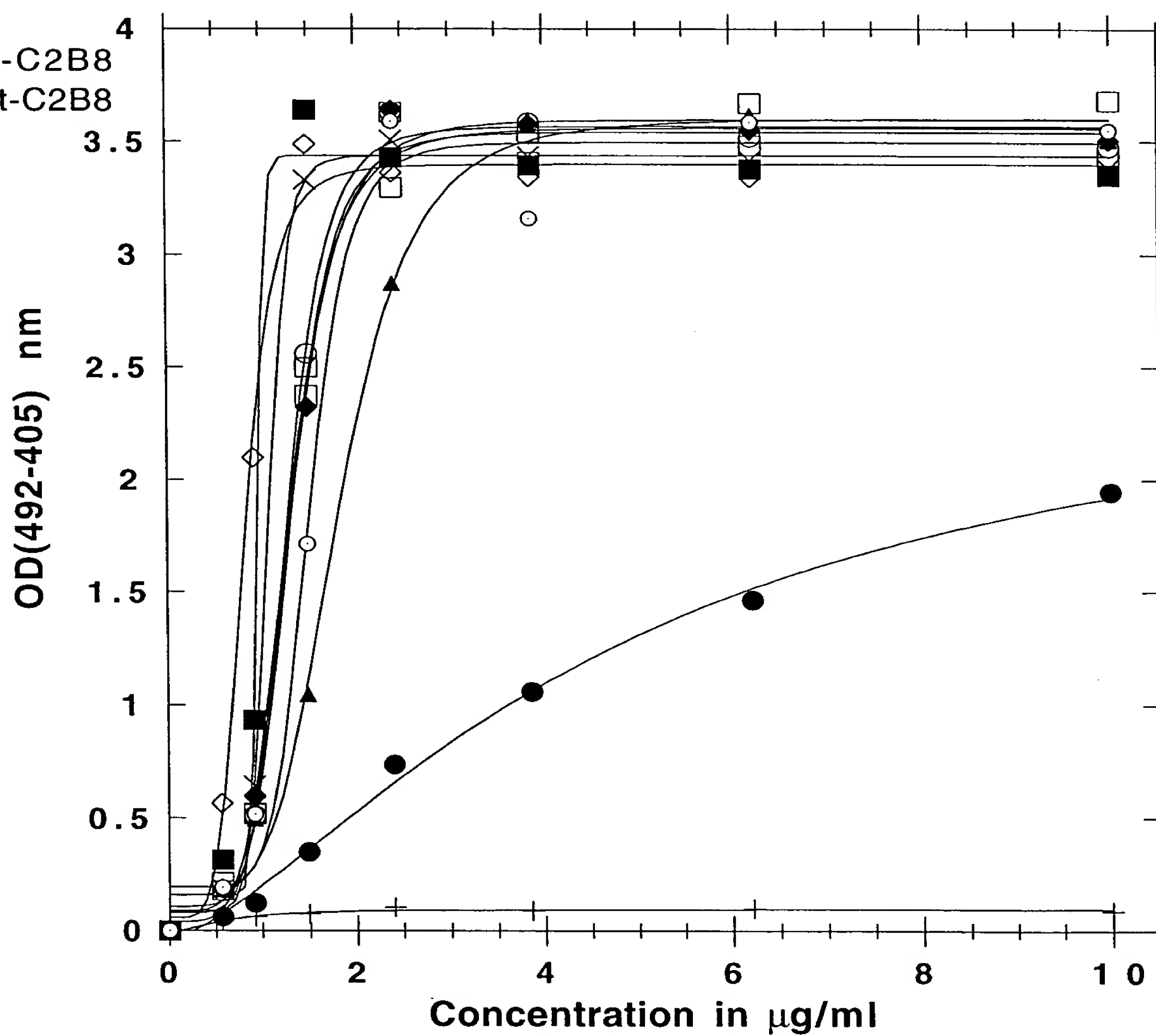


FIG. 8



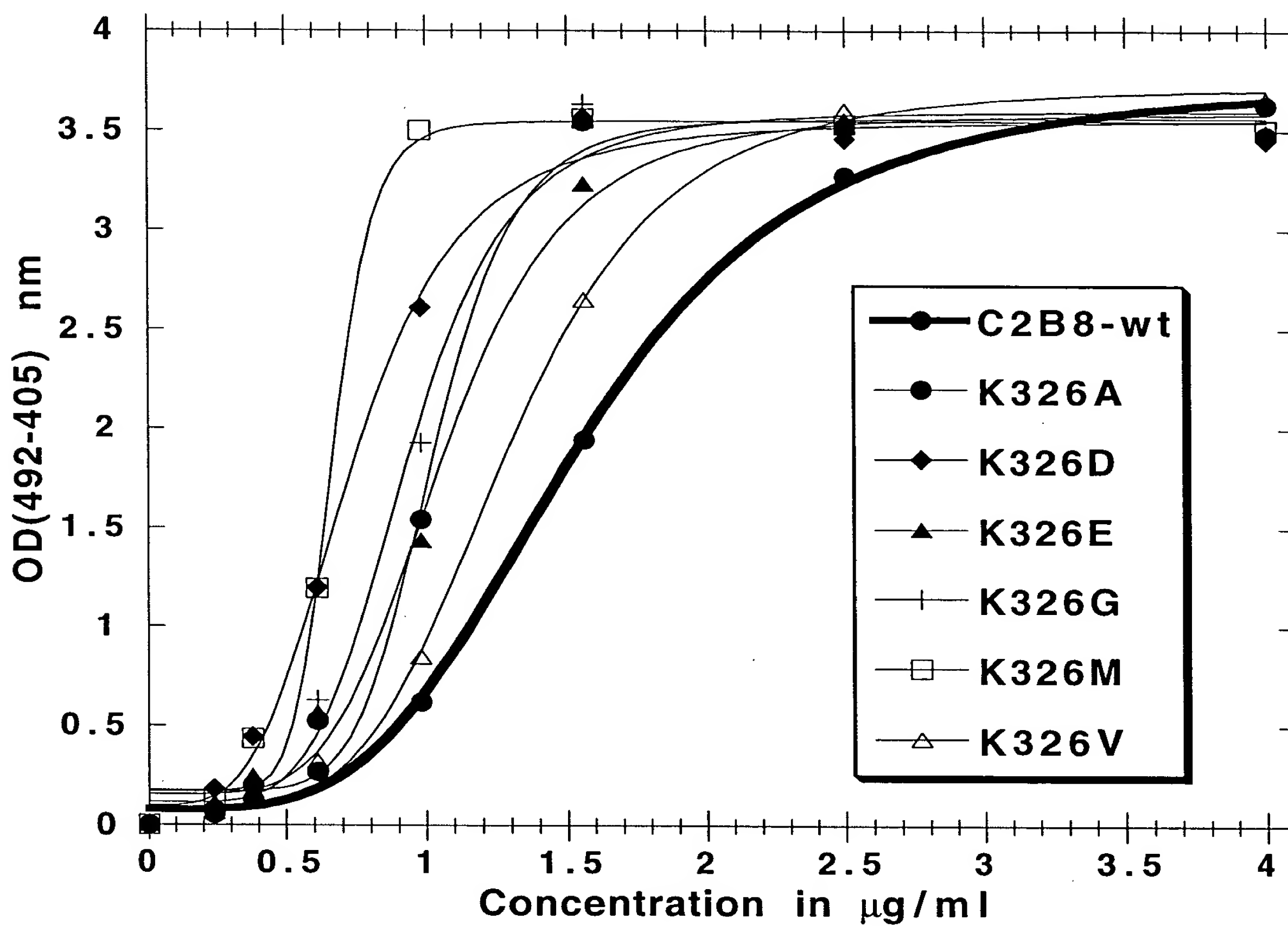


FIG. 9

00470-383460

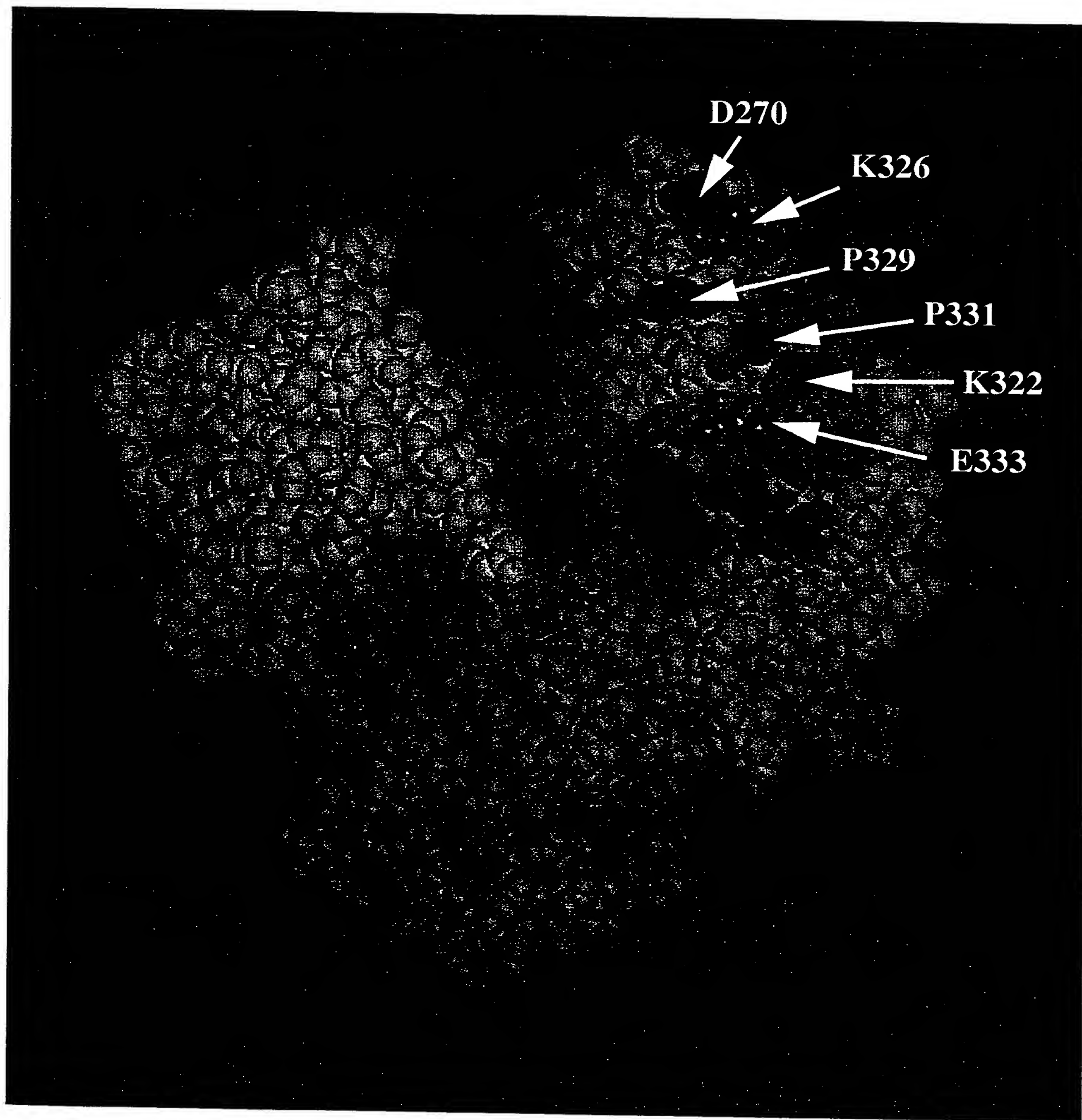


FIG. 10

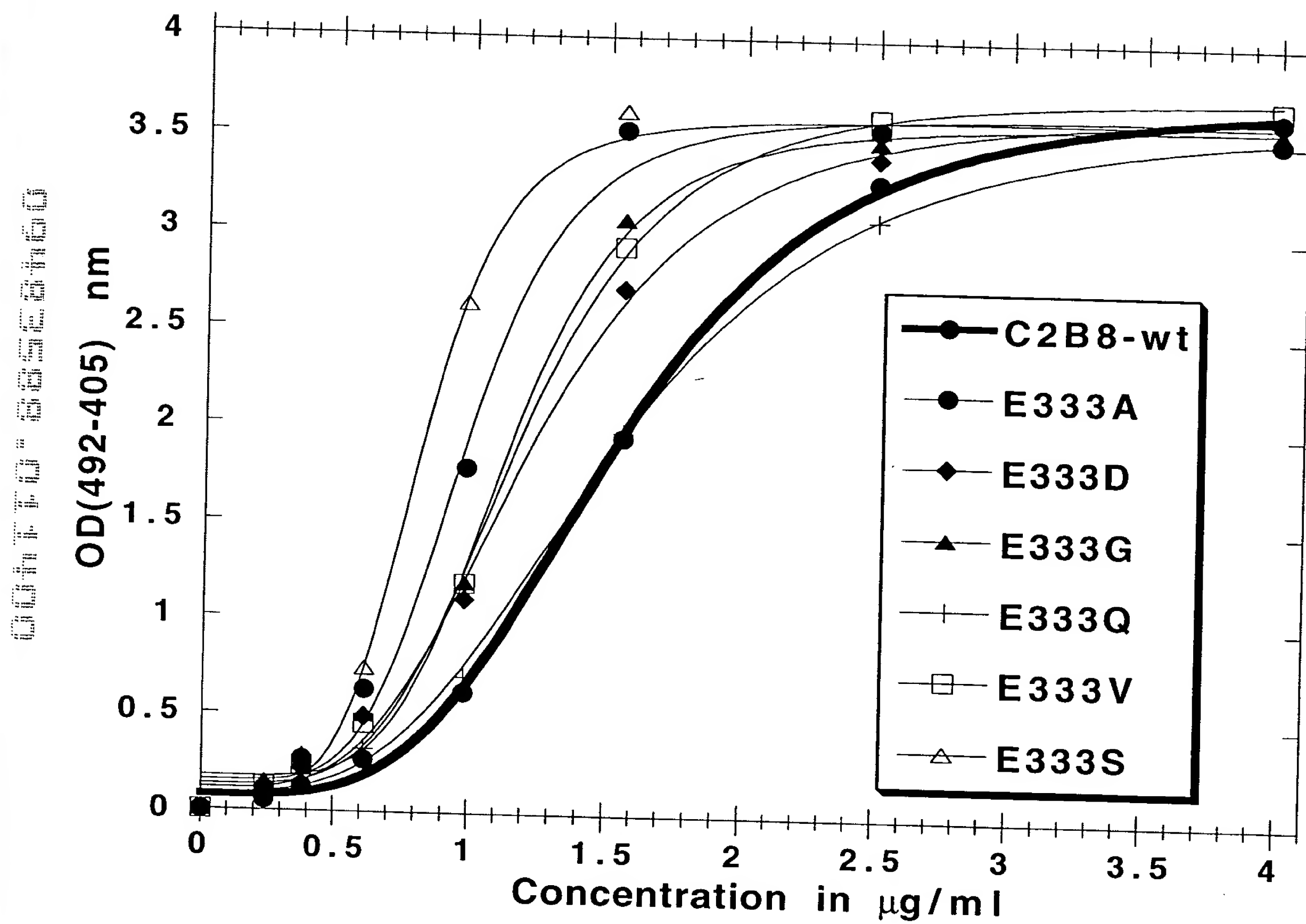


FIG. 11

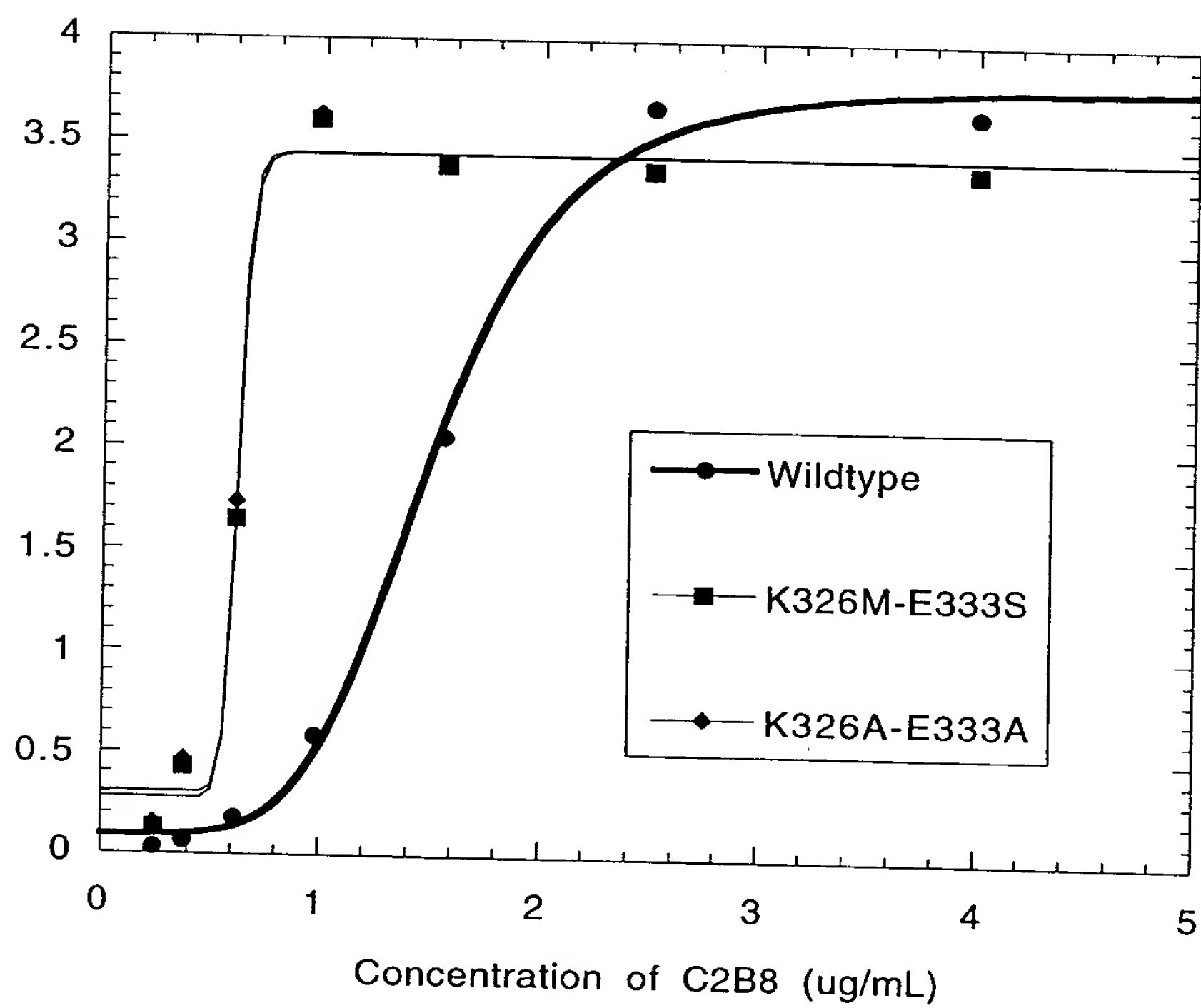


FIG. 12

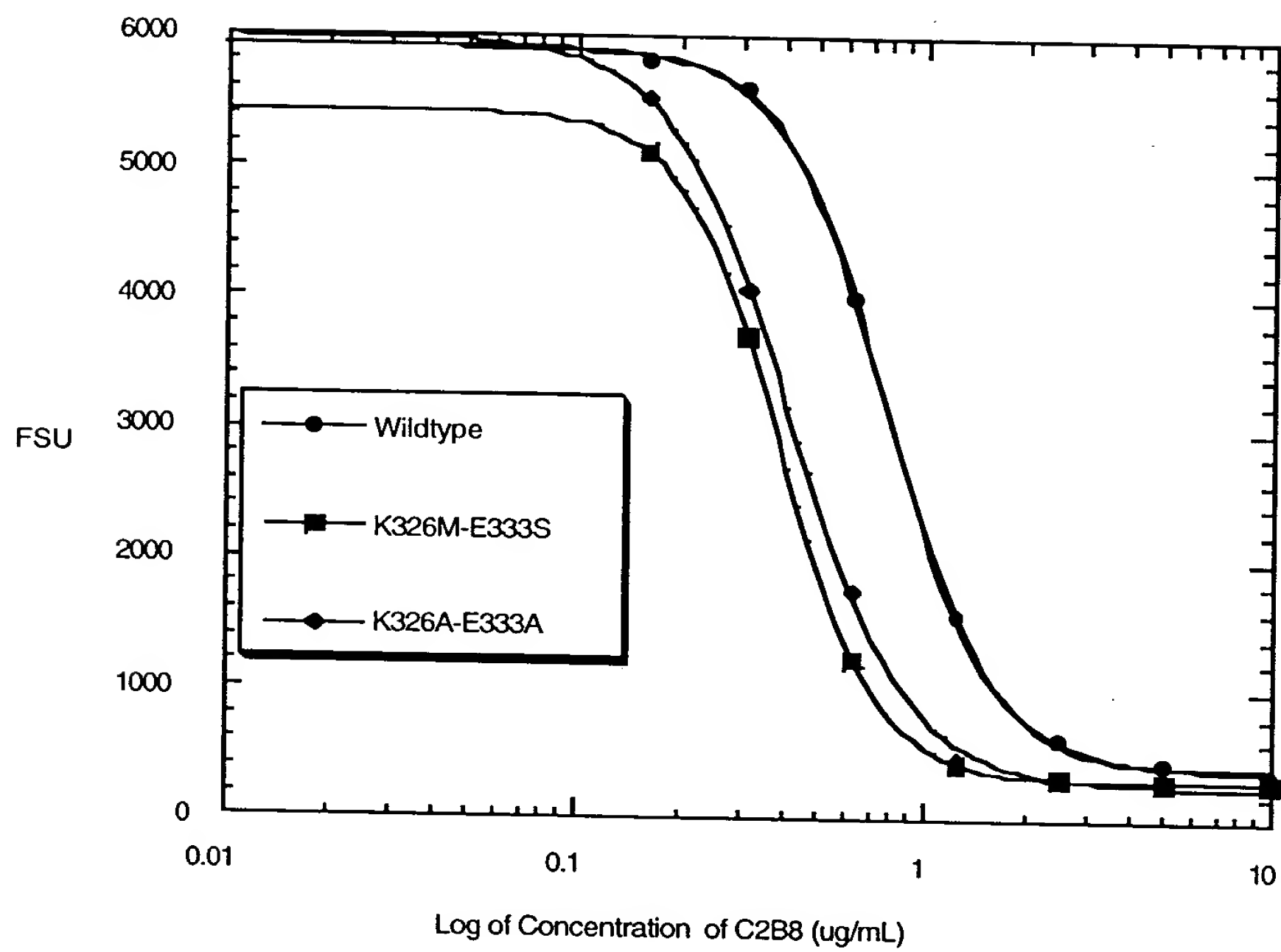
[illegible]

FIG. 13

EC50 of wt-C2B8 = 1.54  
 EC50 of A327g (C2B8) = 1.08

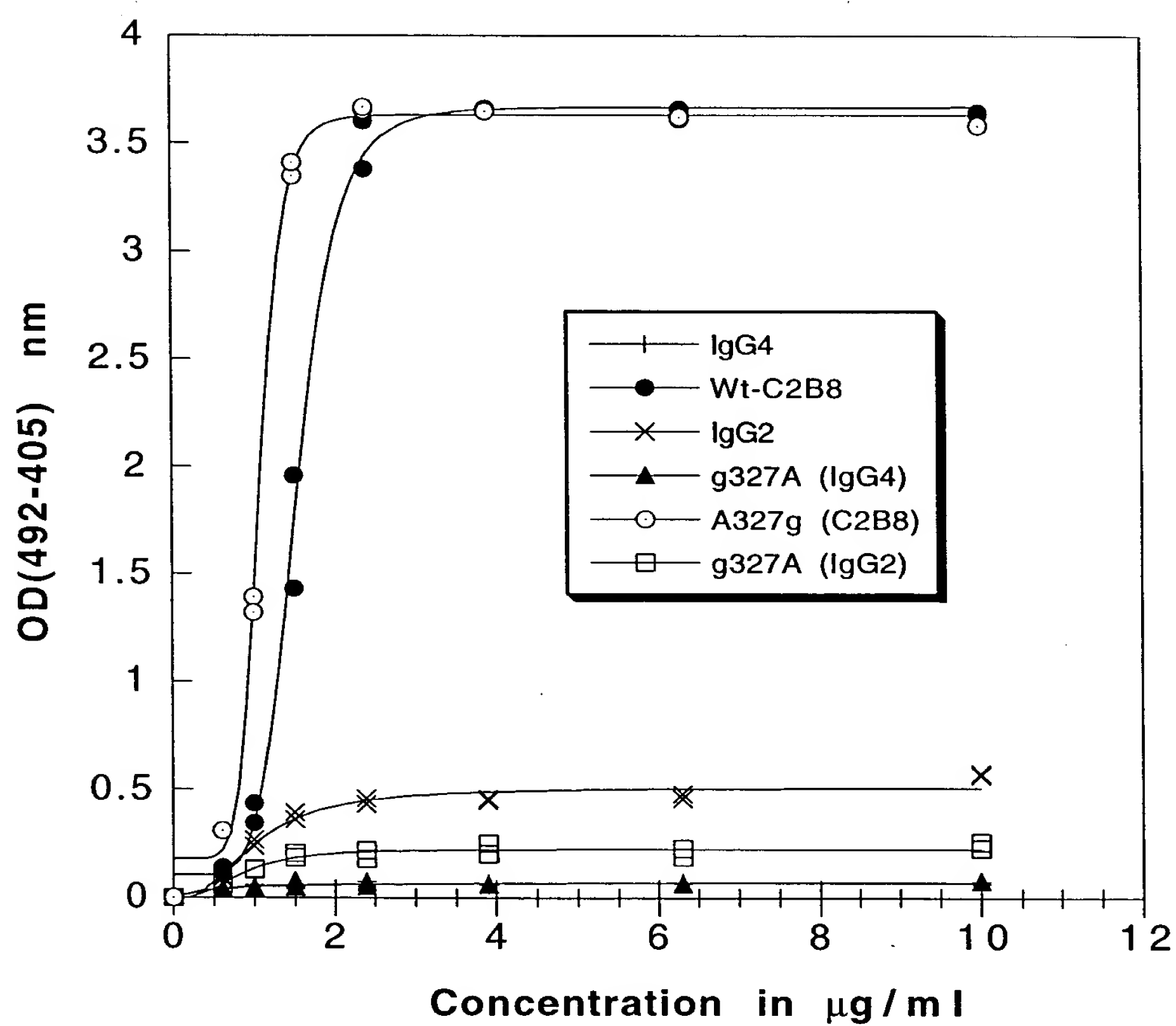


FIG. 14

Fe $\gamma$ R11B

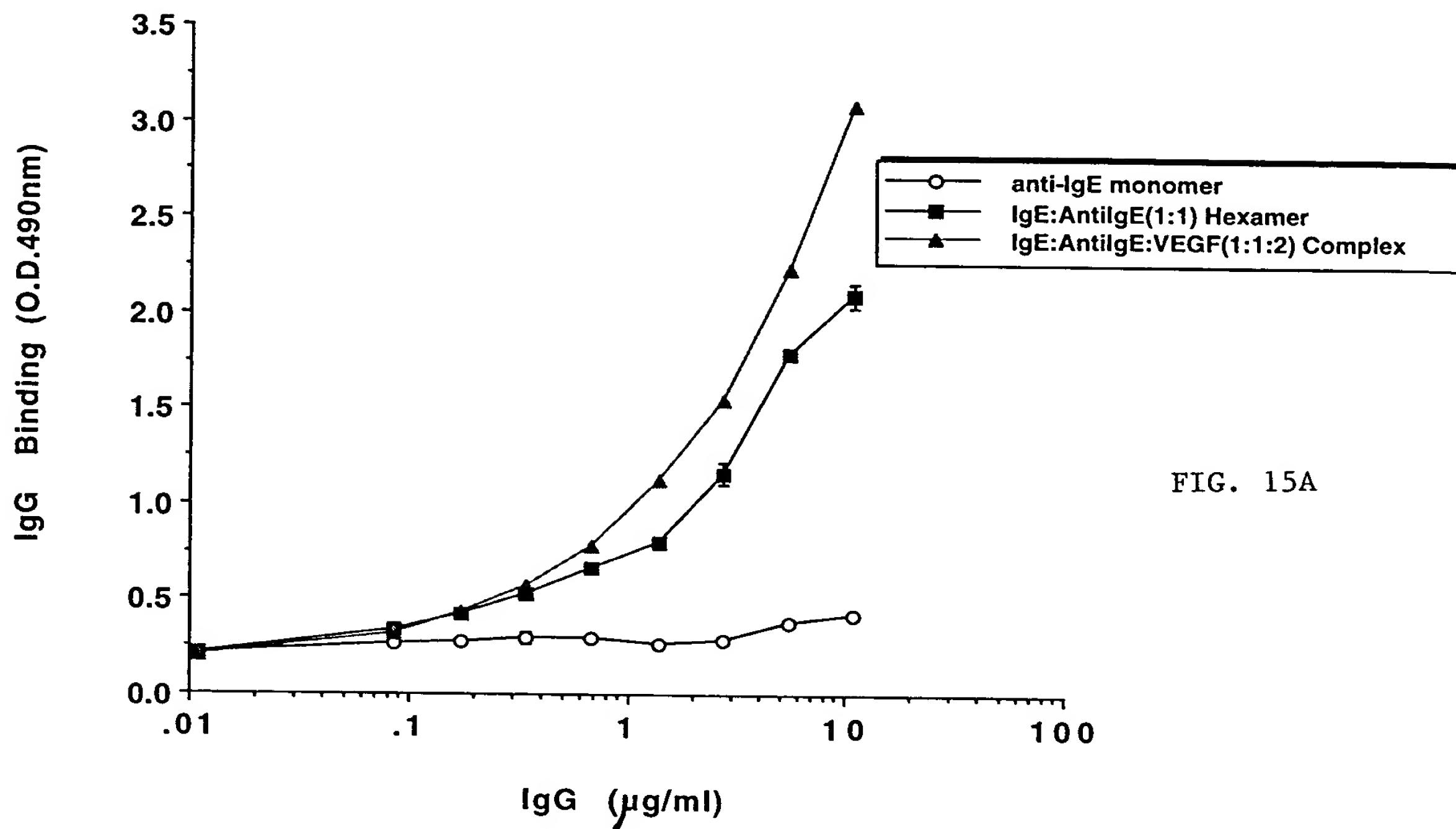


FIG. 15A

Fe $\gamma$ R11A

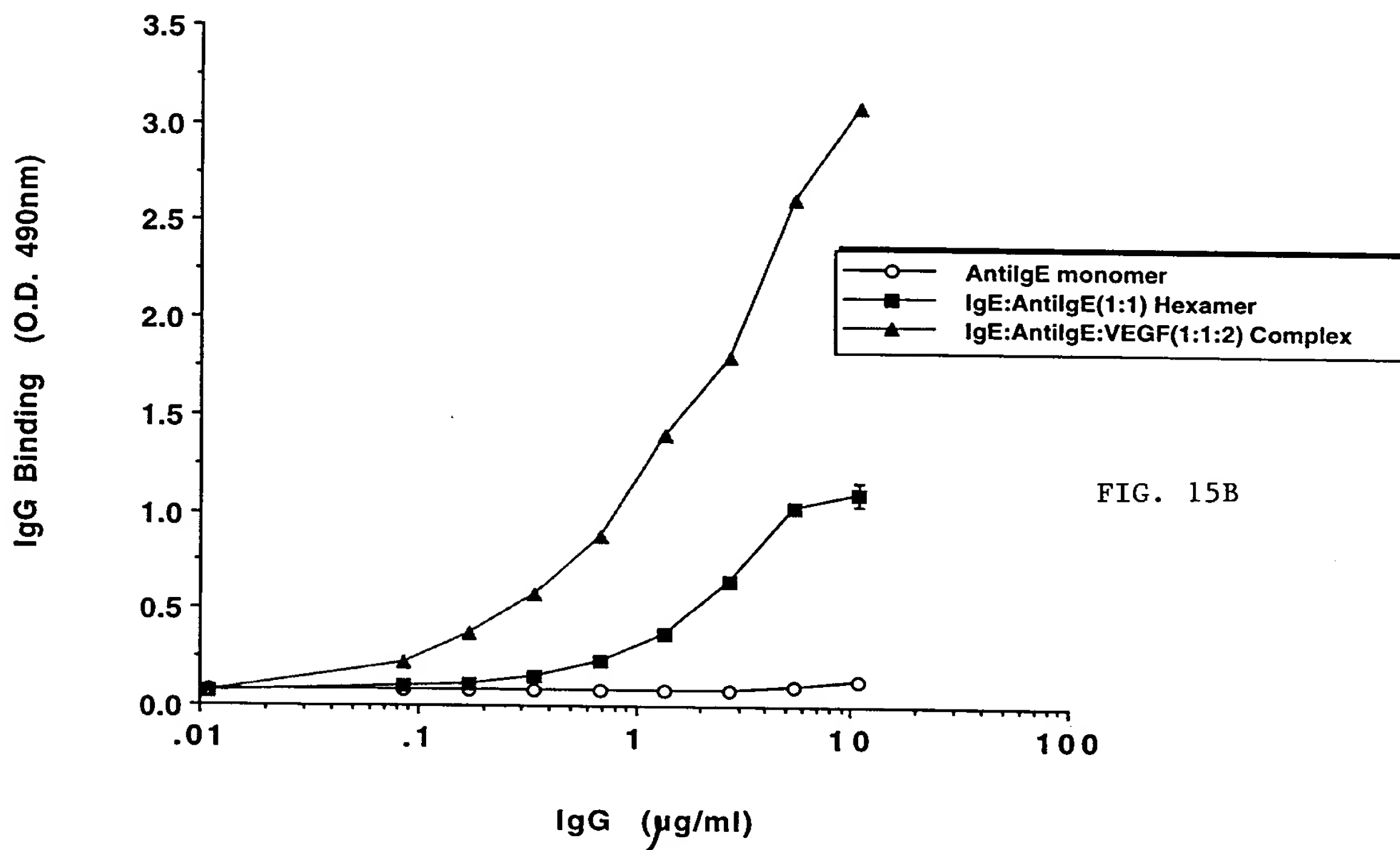


FIG. 15B

FcγRIIA

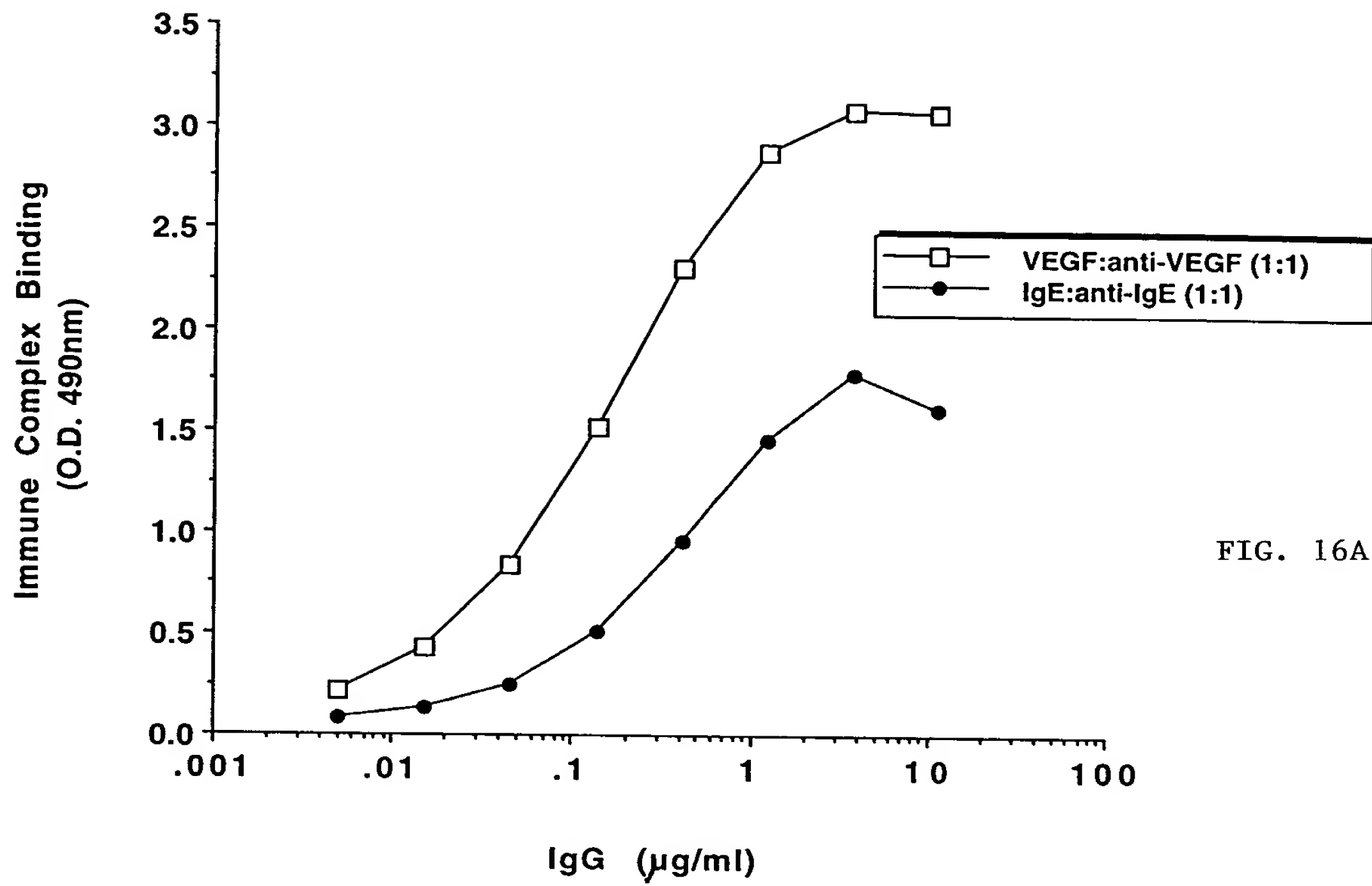


FIG. 16A

FcγRIIA

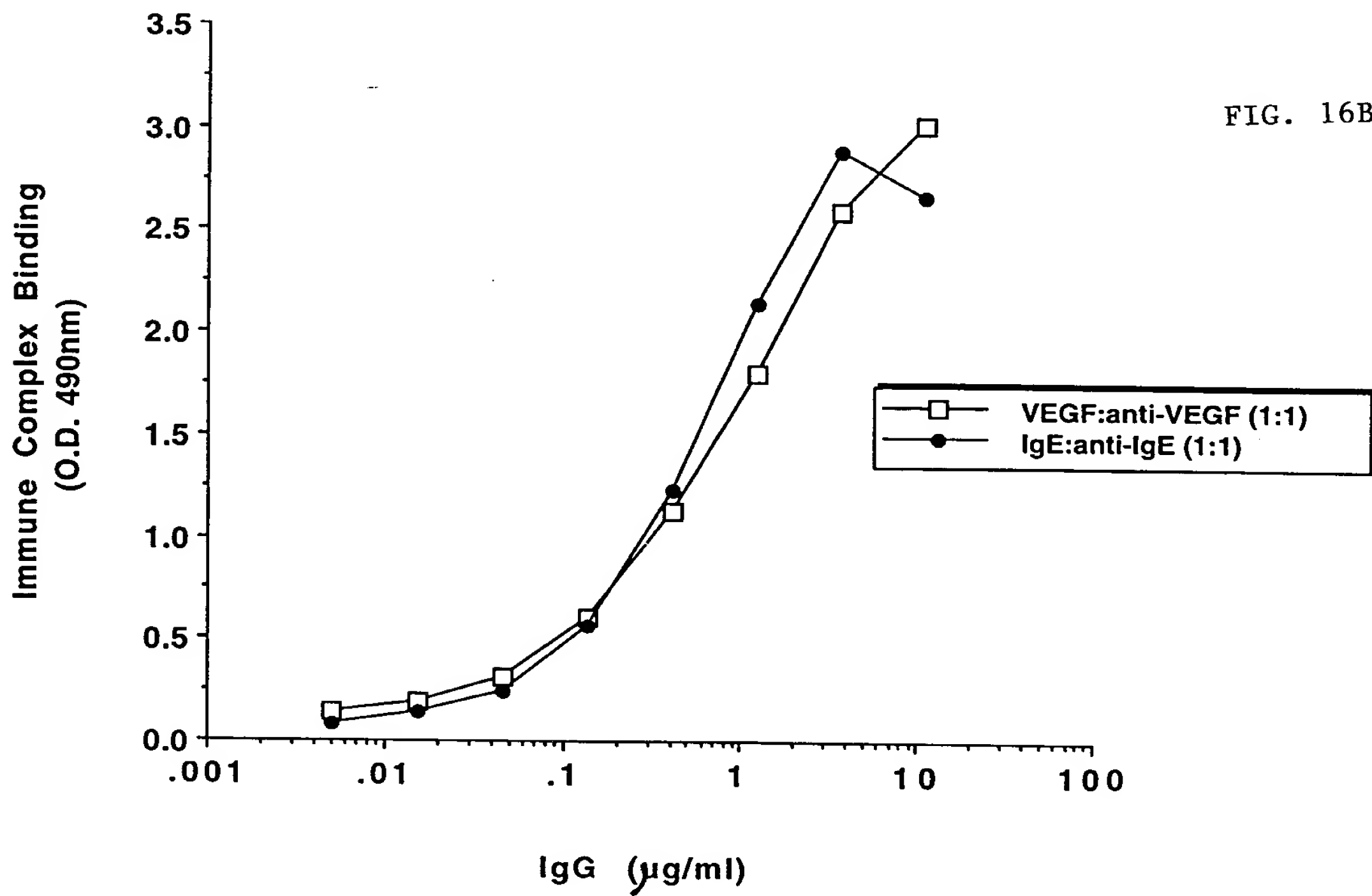


FIG. 16B



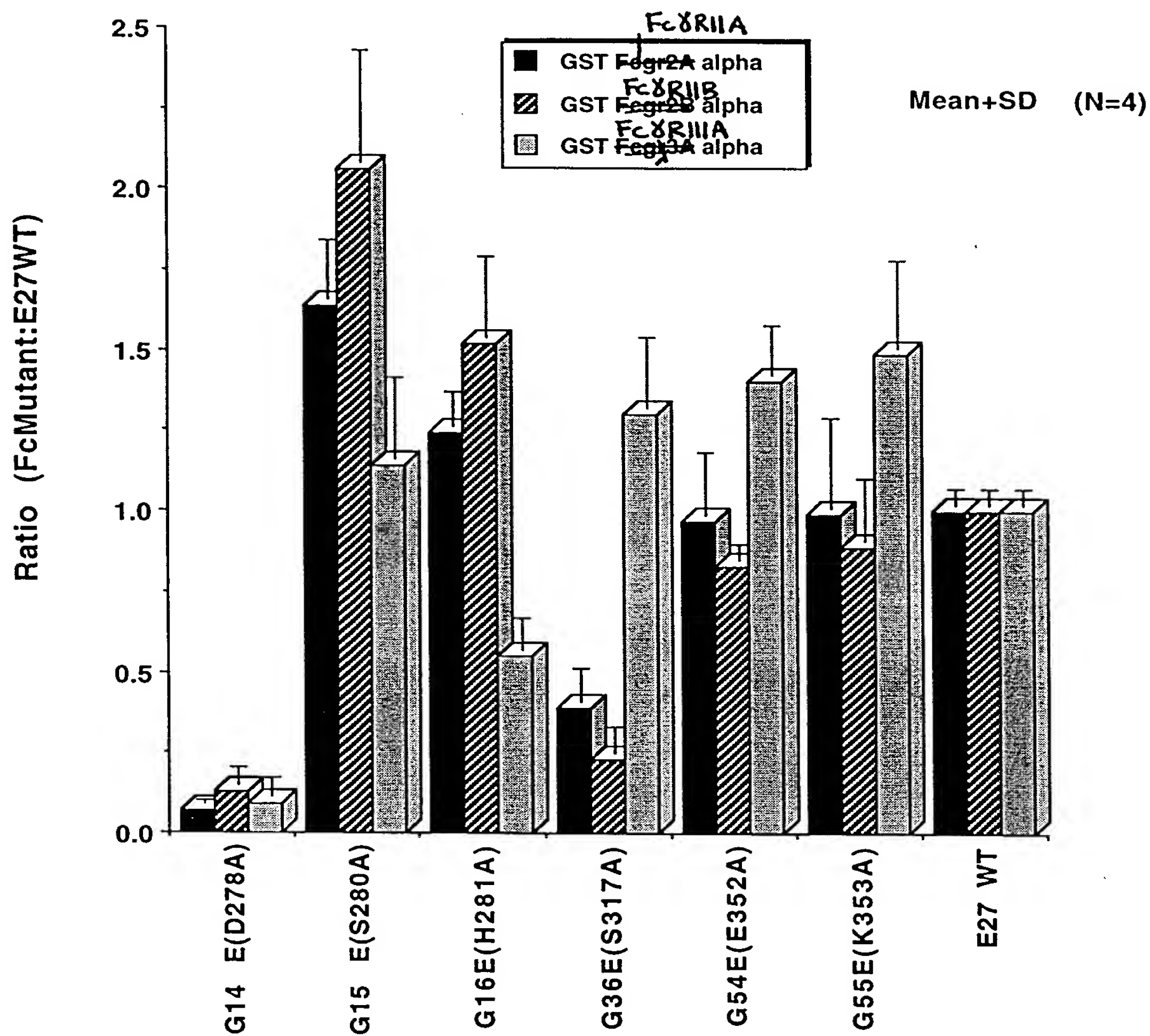


FIG. 17

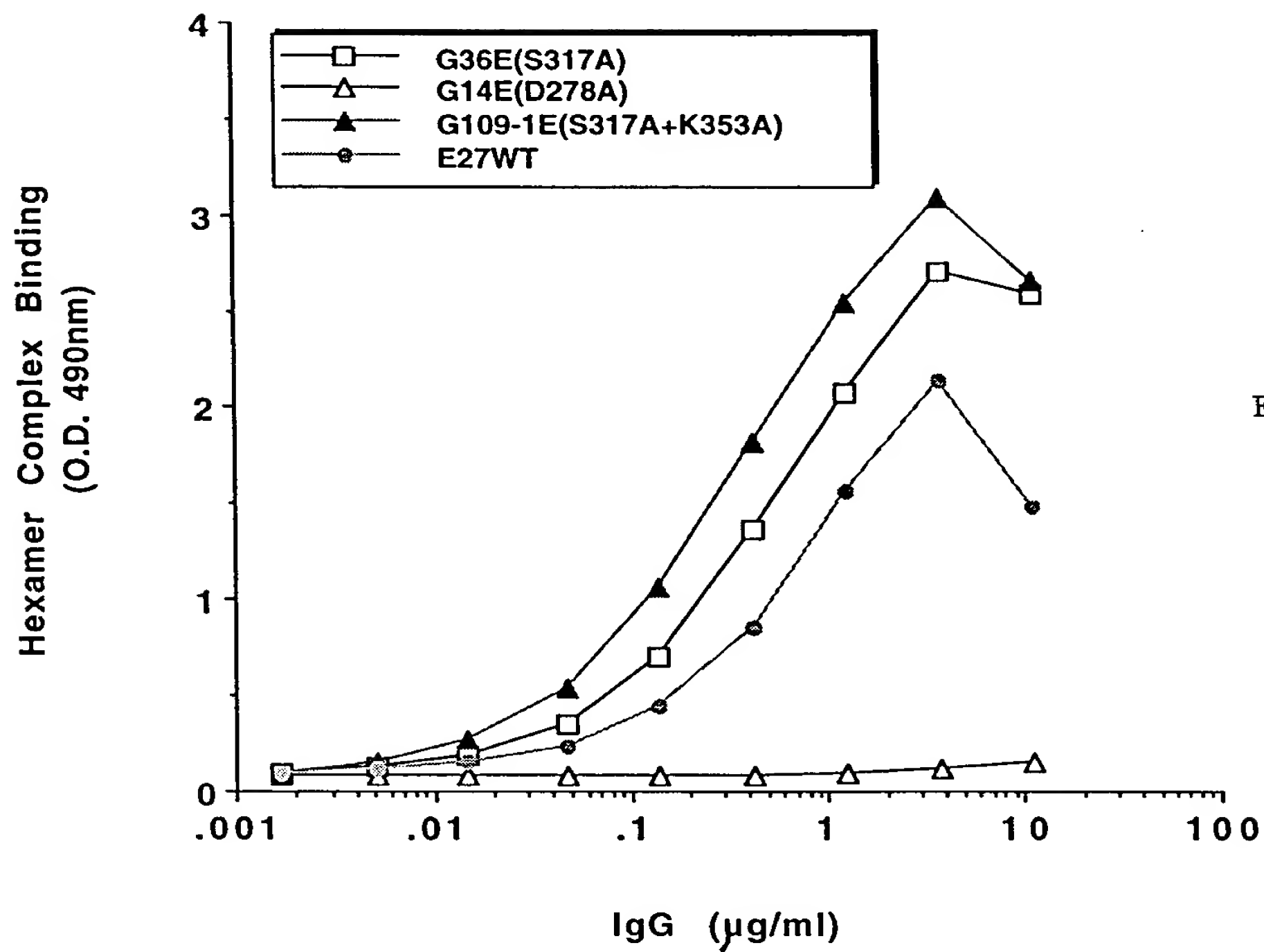


FIG. 18A

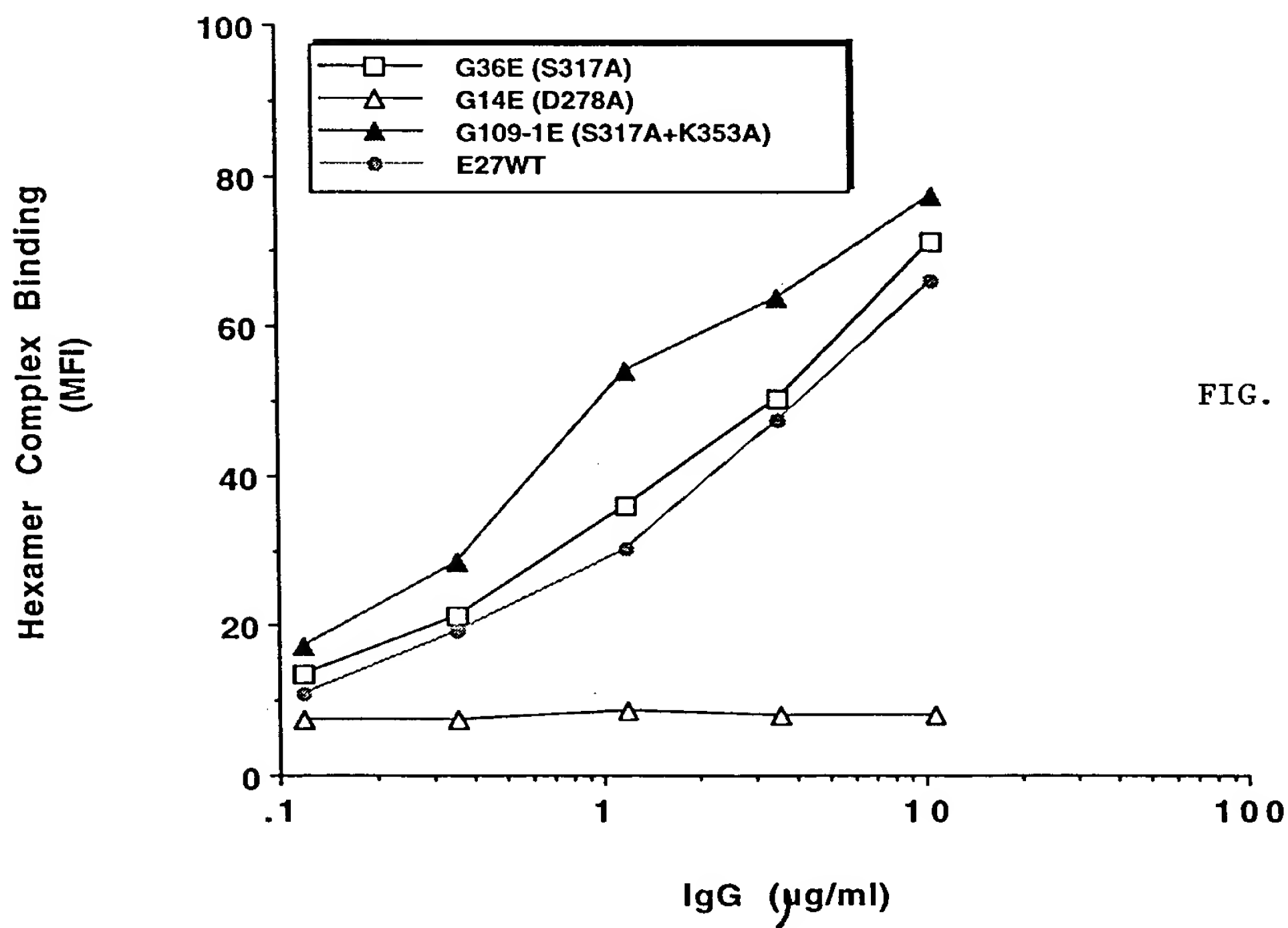


FIG. 18B

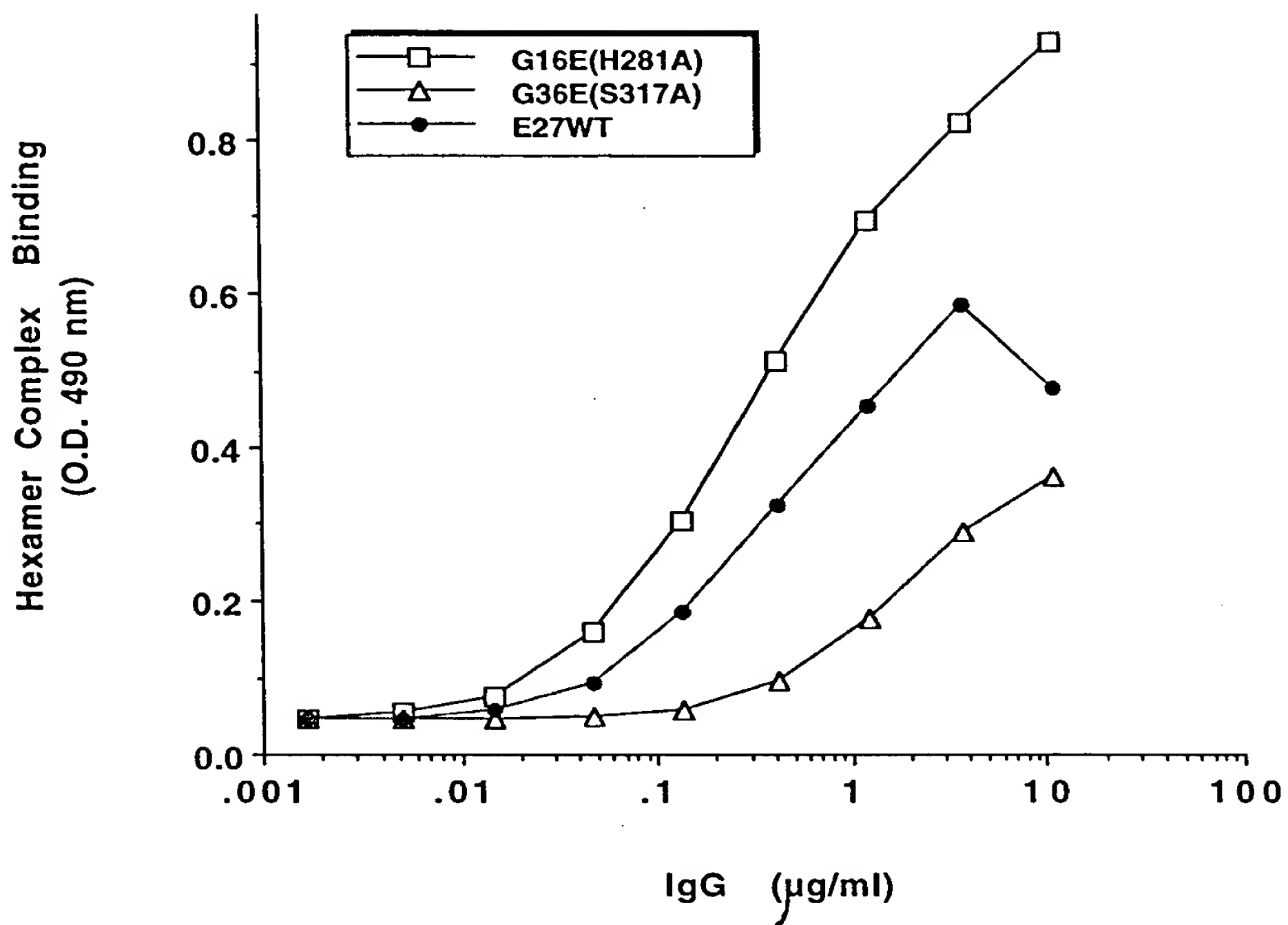


FIG. 19A

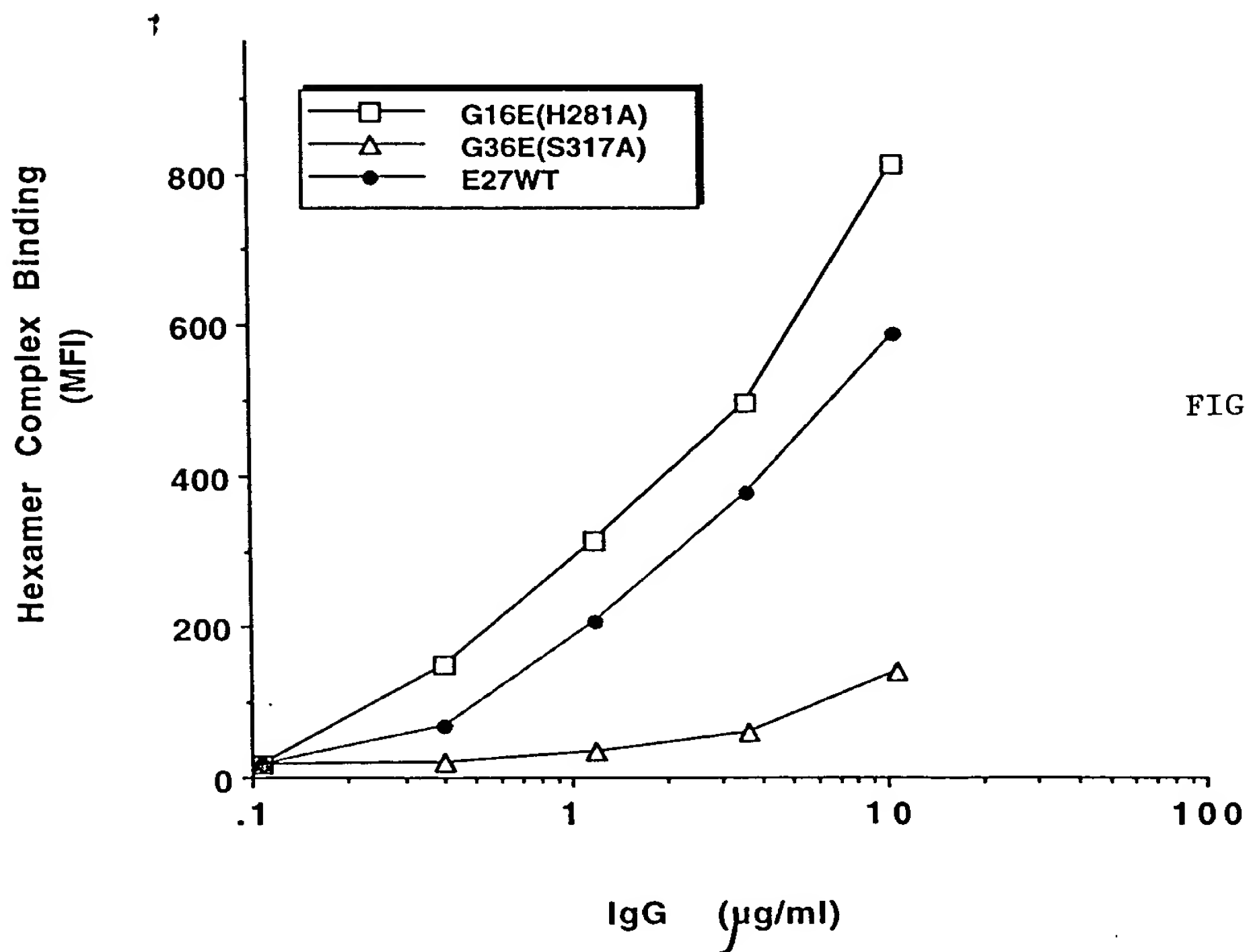


FIG. 19B

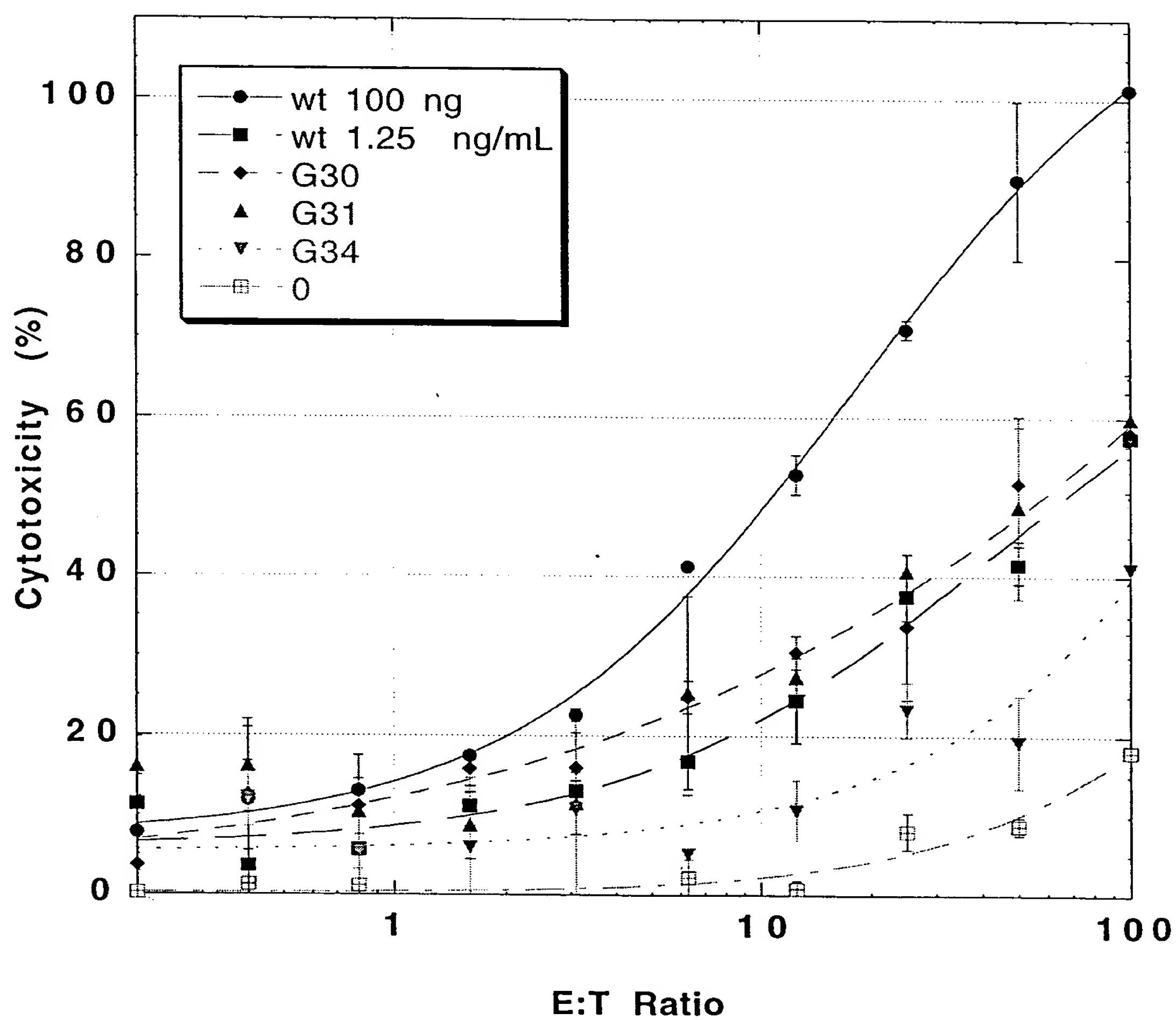


FIG. 20

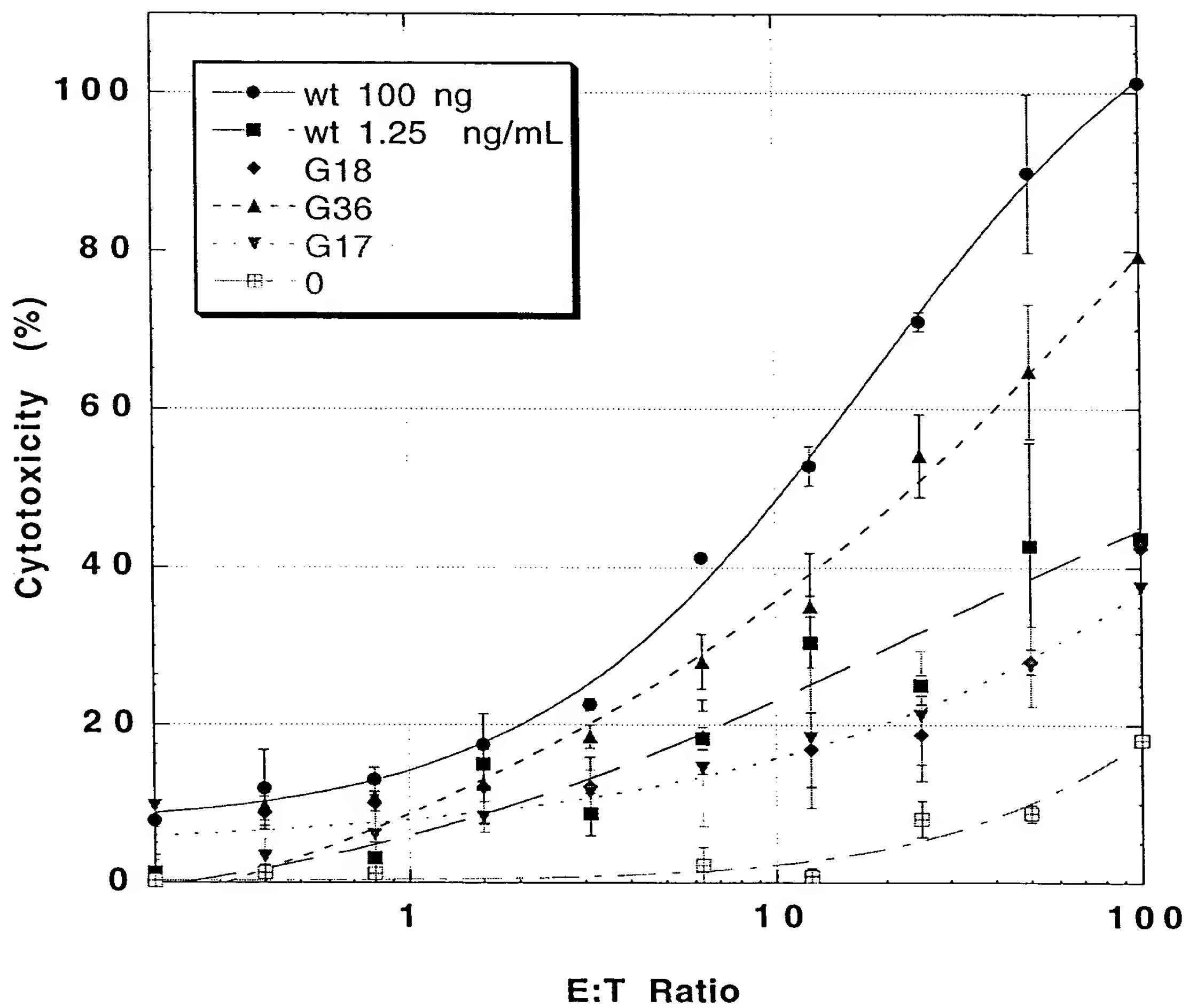


FIG. 21

	230	240	250	260	270
humIgG1	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV				
humIgG2	PAP - PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYV				
humIgG3	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYV				
humIgG4	PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYV				
murIgG1	---TVPEVSSVFIFPPKPKDVLITITLTPKVTCVVVDISKDDPEVQFSWFV				
murIgG2A	PAPNLLGGPSVFIFPPKIKDVLMLISLSPIVTCVVVDVSEDDPDVQISWFV				
murIgG2B	PAPNLEGGPSVFIFPPNIKDVLMLISLTPKVTCVVVDVSEDDPDVQISWFV				
murIgG3	PPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFV				
	280	290	300	310	320
humIgG1	DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP				
humIgG2	DGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLP				
humIgG3	DGVEVHNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALP				
humIgG4	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP				
murIgG1	DDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDCLNGKEFKCRVNSAAFP				
murIgG2A	NNVEVHTAQTQTHREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLP				
murIgG2B	NNVEVHTAQTQTHREDYNSTIRVVSHPILQHODWMSGKEFKCKVNNKDLP				
murIgG3	DNKEVHTAWTQPREAQYNSTFRVVSALPIQHODWMRGKEFKCKVNNKALP				
	330	340	350	360	370
humIgG1	APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV D L				
humIgG2	APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
humIgG3	APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
humIgG4	SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAV				
murIgG1	APIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITV				
murIgG2A	APIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYV				
murIgG2B	SPIERTISKPKGLVRAPQVYTLPPPAEQLSRKDVSLTCLVVGFNPGDISV				
murIgG3	APIERTISKPKGRAQTPQVYTIPPPREQMSKKKVSLTCLVTNFFSEAISV				
	380	390	400	410	420
humIgG1	EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMH				
humIgG2	EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMH				
humIgG3	EWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMH				
humIgG4	EWZSNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSQSVMH				
murIgG1	EWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVNQKSNWEAGNTFTCSVLH				
murIgG2A	EWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVH				
murIgG2B	EWTNNGHTEENYKDTAPVLDSDGSYFIYSKLVNMKTSKWEKTDSEFSCNVRH				
murIgG3	EWERNGELEQDYKNTPPILDSGDYFVYSKLVNMTDSDWLGGEIFTCSVH				
	430	440			
humIgG1	EALHNHYTQKSLSLSPGK				
humIgG2	EALHNHYTQKSLSLSPGK				
humIgG3	EALHNRFTQKSLSLSPGK				
humIgG4	EALHNHYTQKSLSLSPGK				
murIgG1	EGLHNHHTTKSLSHSPGK				
murIgG2A	EGLHNHHTTKSFSRTPGK				
murIgG2B	EGLKNYYLKKTISRSPGK				
murIgG3	EALHNHHTQKNLSRSPGK				

FIG. 22A

Percent Identity Among Fc Sequences

	1	2	3	4	5	6	7	8
1. humIgG1	-	94	94	94	64	66	63	68
2. humIgG2		-	93	92	65	63	60	67
3. humIgG3			-	91	64	64	61	67
4. humIgG4				-	62	64	61	64
5. murIgG1					-	65	61	67
6. murIgG2A						-	77	70
7. murIgG2B							-	68
8. murIgG3								-

FIG. 22B

004470" 8856460

	230	240	250	260	270
humIgG1	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV				
humIgG2	PAP - PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYV				
humIgG3	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYV				
humIgG4	PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV				
	****			*	* *
	280	290	300	310	320
humIgG1	DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP				
humIgG2	DGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLP				
humIgG3	DGVEVHNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALP				
humIgG4	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP				
		*	*	*	*
	330	340	350	360	370
humIgG1	APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
				D L	
humIgG2	APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
humIgG3	APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
humIgG4	SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAV				
	**	*		*	
	380	390	400	410	420
humIgG1	EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH				
humIgG2	EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH				
humIgG3	EWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMH				
humIgG4	EWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH				
	*	*	*	*	* *
	430	440			
humIgG1	EALHNHYTQKSLSLSPGK				
humIgG2	EALHNHYTQKSLSLSPGK				
humIgG3	EALHNRFTQKSLSLSPGK				
humIgG4	EALHNHYTQKSLSLSPGK				
	**	*			

FIG. 23



001110" 32528160

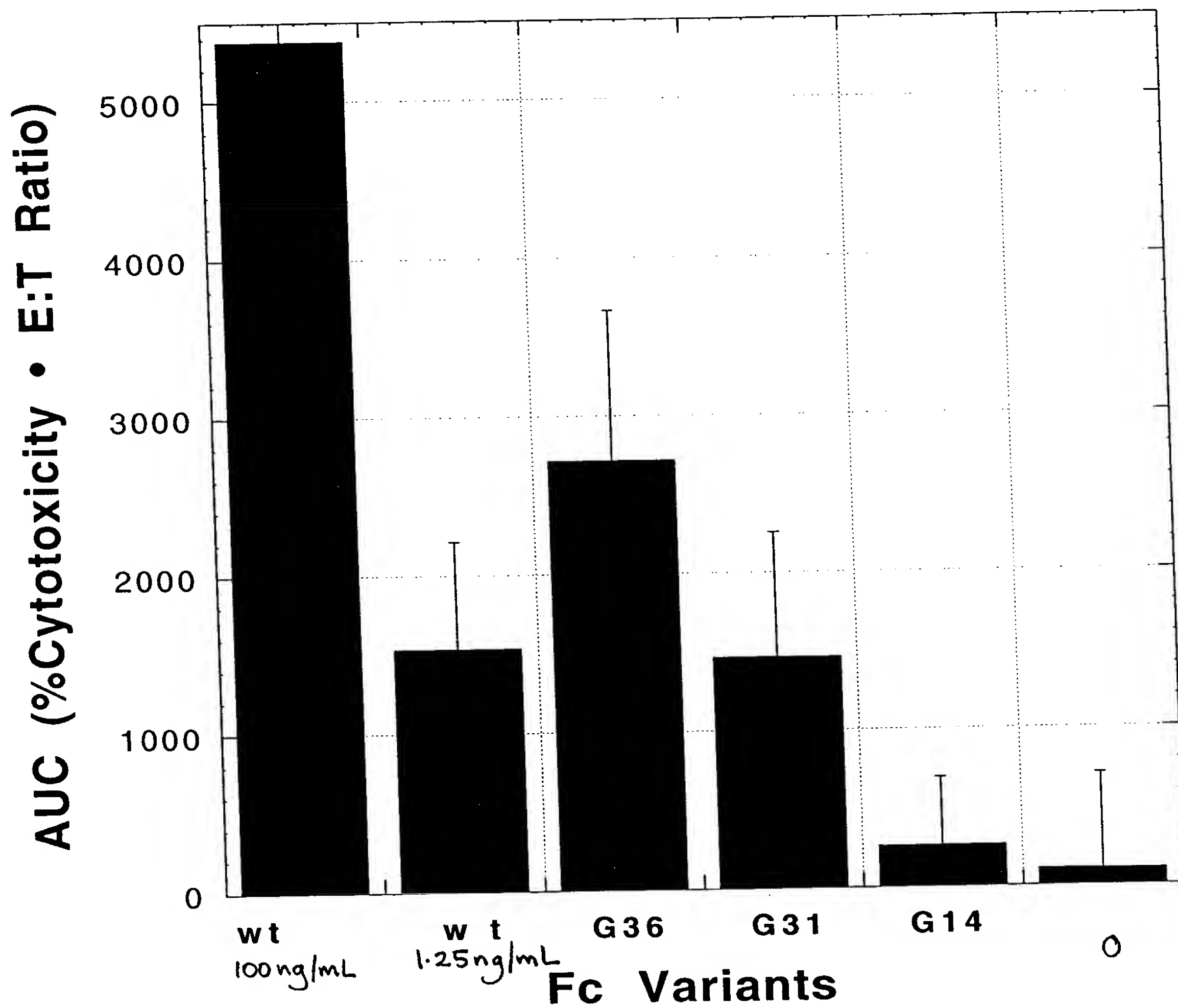


FIG. 24